



SEQUENCE LISTING

<110> AEROVANCE, INC.
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YUNG, Stephanie L.
LONGPHRE, Malinda
WONG, Teresa Mo-fun
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<120> MODIFIED IL-4 MUTEIN RECEPTOR ANTAGONISTS

<130> AERO1210-2

<140> US 10/820,559
<141> 2004-04-08

<150> US 60/530,182
<151> 2003-12-17

<150> US 60/528,228
<151> 2003-12-09

<150> US 60/498,906
<151> 2003-08-29

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<170> PatentIn version 3.3

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actgagaagg aaaccttctg cagggctgcg actgtgctcc ggcagttcta cagccaccat 180
gagaaggaca ctgcgtgcct ggggtgcgact gcacagcagt tccacaggca caagcagctg 240
atccgattcc tgaaacggct cgacaggaac ctctggggcc tggcgggctt gaattcctgt 300
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actgagaagg aaaccttctg cagggctgcg actgtgctcc ggcagttcta cagccaccat      180
gagaaggaca ctgctgcctt ggggtgcgact gcacagcagt tccacaggca caagcagctg      240
atccgattcc tgaaacggct cgacaggaac ctctggggcc tggcgggctt gaattcctgt      300
cctgtgaagg aagccaacca gagtacgttg gaaaacttct tggaaaggct aaagacgata      360
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actgagaagg aaaccttctg cagggctgcg actgtgctcc ggcagttcta cagccaccat      180
gagaaggaca ctgctgcctt ggggtgcgact gcacagcagt tccacaggca caagcagctg      240
atccgattcc tgaaacggct cgacaggaac ctctggggcc tggcgggctt gaattcctgt      300
cctgtgaagg aagccaacca gagtacgttg gaaaacttct tggaaaggct aaagacgata      360
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actgagaagg aaaccttctg cagggctgcg actgtgctcc ggcagttcta cagccaccat      180
gagaaggaca ctgctgcctt ggggtgcgact gcacagcagt tccacaggca caagcagctg      240
atccgattcc tgaaacggct cgacaggaac ctctggggcc tggcgggctt gaattcctgt      300
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 actgagaagg aaaccttctg cagggctgcg actgtgctcc ggcagttcta cagccaccat 180
 gagaaggaca ctgctgcct ggggtgcgact gcacagcagt tccacaggca caagcagctg 240
 atccgattcc tgaaacggct cgacaggaac ctctggggcc tggcgggctt gaattcctgt 300
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 gagaaggaca ctgctgcct ggggtgcgact gcacagcagt tccacaggca caagcagctg 240
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 gagaaggaca ctgctgcct ggggtgcgact gcacagcagt tccacaggca caagcagctg 240
 atccgattcc tgaaacggct cgacaggaac ctctggggcc tggcgggctt gaattcctgt 300
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 actgagaagg aaaccttctg cagggctgcg actgtgctcc ggcagttcta cagccaccat 180
 gagaaggaca ctgctgcct ggggtgcgact gcacagcagt tccacaggca caagcagctg 240
 atccgattcc tgaaacggct cgacaggaac ctctggggcc tggcgggctt gaattcctgt 300
 cctgtgaagg aagccaactg cagtacgttg gaaaacttct tggaaaggct aaagacgatc 360
 atggacgaga aagactcaaa gtgttcgagc taataa 396

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 <212> PRT
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 Met His Lys Cys Asp Ile Thr Leu Gln Glu Ile Ile Lys Thr Leu Asn
 1 5 10 15
 Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu Thr Val Thr Asp
 20 25 30
 Ile Phe Ala Ala Ser Lys Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg
 35 40 45

Ala Ala Thr Val Leu Arg Gln Phe Tyr Ser His His Glu Lys Asp Thr
 50 55 60

Arg Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln Leu
 65 70 75 80

Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly
 85 90 95

Leu Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser Thr Leu Glu Asn
 100 105 110

Phe Leu Glu Arg Leu Lys Thr Ile Met Asp Glu Lys Asp Ser Lys Cys
 115 120 125

Ser Ser
 130

<210> 10

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<400> 10

Met His Lys Cys Asp Ile Thr Leu Gln Glu Ile Ile Lys Thr Leu Asn
 1 5 10 15

Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu Cys Val Thr Asp
 20 25 30

Ile Phe Ala Ala Ser Lys Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg
 35 40 45

Ala Ala Thr Val Leu Arg Gln Phe Tyr Ser His His Glu Lys Asp Thr
 50 55 60

Arg Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln Leu
 65 70 75 80

Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly
 85 90 95

Leu Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser Thr Leu Glu Asn
 100 105 110

Phe Leu Glu Arg Leu Lys Thr Ile Met Asp Glu Lys Asp Ser Lys Cys
 115 120 125

Ser Ser
 130

<210> 11
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<400> 11

Met His Lys Cys Asp Ile Thr Leu Gln Glu Ile Ile Lys Thr Leu Asn
 1 5 10 15

Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu Thr Val Thr Asp
 20 25 30

Ile Phe Ala Ala Cys Lys Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg
 35 40 45

Ala Ala Thr Val Leu Arg Gln Phe Tyr Ser His His Glu Lys Asp Thr
 50 55 60

Arg Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln Leu
 65 70 75 80

Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly
 85 90 95

Leu Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser Thr Leu Glu Asn
 100 105 110

Phe Leu Glu Arg Leu Lys Thr Ile Met Asp Glu Lys Asp Ser Lys Cys
 115 120 125

Ser Ser
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<210> 12
 <211> 130
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<400> 12

Met	His	Lys	Cys	Asp	Ile	Thr	Leu	Gln	Glu	Ile	Ile	Lys	Thr	Leu	Asn
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Ser	Leu	Thr	Glu	Gln	Lys	Thr	Leu	Cys	Thr	Glu	Leu	Thr	Val	Thr	Asp
			20					25					30		

Ile	Phe	Ala	Ala	Ser	Cys	Asn	Thr	Thr	Glu	Lys	Glu	Thr	Phe	Cys	Arg
		35					40					45			

Ala	Ala	Thr	Val	Leu	Arg	Gln	Phe	Tyr	Ser	His	His	Glu	Lys	Asp	Thr
		50				55					60				

Arg	Cys	Leu	Gly	Ala	Thr	Ala	Gln	Gln	Phe	His	Arg	His	Lys	Gln	Leu
65						70				75					80

Ile	Arg	Phe	Leu	Lys	Arg	Leu	Asp	Arg	Asn	Leu	Trp	Gly	Leu	Ala	Gly
				85					90					95	

Leu	Asn	Ser	Cys	Pro	Val	Lys	Glu	Ala	Asn	Gln	Ser	Thr	Leu	Glu	Asn
			100					105					110		

Phe	Leu	Glu	Arg	Leu	Lys	Thr	Ile	Met	Asp	Glu	Lys	Asp	Ser	Lys	Cys
		115					120					125			

Ser	Ser
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<210> 13

<211> 130

<212> PRT

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<220>

<223> Modified human sequence

<400> 13

Met	His	Lys	Cys	Asp	Ile	Thr	Leu	Gln	Glu	Ile	Ile	Lys	Thr	Leu	Asn
1				5					10					15	

Ser	Leu	Thr	Glu	Gln	Lys	Thr	Leu	Cys	Thr	Glu	Leu	Thr	Val	Thr	Asp
			20					25					30		

Ile	Phe	Ala	Ala	Ser	Lys	Cys	Thr	Thr	Glu	Lys	Glu	Thr	Phe	Cys	Arg
		35					40					45			

Ala Ala Thr Val Leu Arg Gln Phe Tyr Ser His His Glu Lys Asp Thr
 50 55 60

Arg Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln Leu
 65 70 75 80

Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly
 85 90 95

Leu Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser Thr Leu Glu Asn
 100 105 110

Phe Leu Glu Arg Leu Lys Thr Ile Met Asp Glu Lys Asp Ser Lys Cys
 115 120 125

Ser Ser
 130

<210> 14
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 <212> PRT
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<400> 14

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Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu Thr Val Thr Asp
 20 25 30

Ile Phe Ala Ala Ser Lys Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg
 35 40 45

Ala Ala Thr Val Leu Arg Gln Phe Tyr Ser His His Glu Lys Asp Thr
 50 55 60

Arg Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln Leu
 65 70 75 80

Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly
 85 90 95

Leu Asn Ser Cys Pro Val Lys Glu Cys Asn Gln Ser Thr Leu Glu Asn

100 105 110

Phe Leu Glu Arg Leu Lys Thr Ile Met Asp Glu Lys Asp Ser Lys Cys
 115 120 125

Ser Ser
 130

<210> 15
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<400> 15

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 1 5 10 15

Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu Thr Val Thr Asp
 20 25 30

Ile Phe Ala Ala Ser Lys Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg
 35 40 45

Ala Ala Thr Val Leu Arg Gln Phe Tyr Ser His His Glu Lys Asp Thr
 50 55 60

Arg Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln Leu
 65 70 75 80

Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly
 85 90 95

Leu Asn Ser Cys Pro Val Lys Glu Ala Cys Gln Ser Thr Leu Glu Asn
 100 105 110

Phe Leu Glu Arg Leu Lys Thr Ile Met Asp Glu Lys Asp Ser Lys Cys
 115 120 125

Ser Ser
 130

<210> 16
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Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu Thr Val Thr Asp
 20 25 30

Ile Phe Ala Ala Ser Lys Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg
 35 40 45

Ala Ala Thr Val Leu Arg Gln Phe Tyr Ser His His Glu Lys Asp Thr
 50 55 60

Arg Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln Leu
 65 70 75 80

Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly
 85 90 95

Leu Asn Ser Cys Pro Val Lys Glu Ala Asn Cys Ser Thr Leu Glu Asn
 100 105 110

Phe Leu Glu Arg Leu Lys Thr Ile Met Asp Glu Lys Asp Ser Lys Cys
 115 120 125

Ser Ser
 130

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<211> 42

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<213> Artificial sequence

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<223> Amplification primer

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42

<210> 18

<211> 42

<212> DNA

<213> Artificial sequence

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<210> 19
<211> 39
<212> DNA
<213> Artificial sequence

<220>
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<400> 19
gtaacagaca tcttttgctgc ctgcaagaac acaactgag 39

<210> 20
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<212> DNA
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<210> 21
<211> 45
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<210> 22
<211> 45
<212> DNA
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<210> 25
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<210> 26
 <211> 41
 <212> DNA
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<220>
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<400> 26
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<220>
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<210> 28
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<400> 28

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44

<210> 30

<211> 44

<212> DNA

<213> Artificial sequence

<220>

<223> Amplification primer

<400> 30

gaagttttcc aacgtactgc agttggcttc cttcacagga cagg

44